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<110> HAYASHIZAKI, Yoshihide
WATAHIKI, Masanori

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<140> US 09/254,344
<141> 1999-09-03

<150> PCT/JP98/03037
<151> 1998-07-06

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310

315

320

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Val Ala Asn Val Ile Thr Lys Trp Lys His Cys Pro Val Glu Asp Ile
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Pro Tyr Asn Met Asp Trp Arg Gly Arg Val Tyr Ala Val Ser Met Phe
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Pro	Ala	Ile	Asp	Ser	Gly	Lys	Gly	Leu	Met	Phe	Thr	Gln	Pro	Asn	Gln
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Ser Gln Asp Gly Ser His Leu Arg Lys Thr Val Val Trp Ala His Glu
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Val Asp Thr Tyr Glu Ser Cys Asp Val Leu Ala Asp Phe Tyr Asp Gln
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Phe Ala Asp Gln Leu His Glu Ser Gln Leu Asp Lys Met Pro Ala Leu
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Ala Arg Phe Arg Lys Met Phe Glu Arg Gln Leu Lys Ala Gly Glu Val
 50 55 60

Ala Asp Asn Ala Ala Lys Pro Leu Ile Thr Thr Lys Met Ile Ala
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Arg Ile Asn Asp Trp Phe Glu Glu Val Lys Ala Lys Arg Gly Lys Arg
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Pro Thr Ala Phe Gln Phe Leu Gln Glu Ile Lys Pro Glu Ala Val Ala

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Phe Gly Arg Ile Arg Asp Leu Glu Ala Lys His	Phe Lys Lys Asn Val		
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Met Gln Val Val Glu Ala Asp Met	Leu Ser Lys Gly Leu Leu Gly Gly		
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Arg Met Leu Ile Glu Ser Thr Gly Met Val Ser	Leu His Arg Gln Asn		
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Glu Asp Ile Asp Met Asn Pro Glu Ala Leu	Thr Ala Trp Lys Arg Ala		
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Pro Leu Glu Asn Thr Ile Trp Trp Ala Glu Gln Asp Ser Pro Phe Ala		
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Val Thr Asp Glu Asn Thr Gly Glu Ile Ser Glu Lys Val Lys Leu Gly		
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Thr Lys Ala Leu Ala Gly Gln Trp Leu Ala Tyr Gly Val Thr Arg Ser		
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Gly Phe Arg Gln Gln Val Leu Glu Asp Thr Ile Gln Pro Ala Ile Asp		
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640		
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Val Thr Pro Asp Gly Phe Pro Val Trp Gln Glu Pro Ile Gln Thr Arg		

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Thr Asn Lys Asp Ser Glu Ile Asp Ala His Lys Gln Glu Ser Gly Ile			
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Ala Pro Asn Phe Val His Ser Gln Asp Gly Ser His Leu Arg Lys Thr			
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Val Val Trp Ala His Glu Lys Tyr Gly Ile Glu Ser Phe Ala Leu Ile			
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His Asp Ser Phe Gly Thr Ile Pro Ala Asn Leu Phe Lys Ala Val Arg			
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805	810	815	
Tyr Asp Gln Phe Ala Asp Gln Leu His Glu Ser Gln Leu Asp Lys Met			
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Ile Ala Asp Asn Ala Ala Lys Pro Leu Leu Ala Thr Lys Leu Thr			
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Thr Arg Ile Val Glu Trp Leu Glu Glu Tyr Ala Ser Lys Lys Gly Arg			
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Lys Pro Ser Ala Tyr Ala Pro Leu Gln Leu Leu Lys Pro Glu Ala Ser			
100	105	110	

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 Met Thr Thr Ile Gln Ala Met Leu Gly Lys Ala Ile Glu Asp Glu Ala
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 Val Glu Glu Gln Leu Asn Lys Arg His Gly Gln Val Tyr Lys Lys Ala
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 Phe Met Gln Val Val Glu Ala Asp Met Ile Gly Arg Gly Leu Leu Gly
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 Gly Glu Ala Trp Ser Ser Trp Asp Lys Glu Thr Thr Met His Val Gly
 195 200 205
 Ile Arg Met Leu Ile Glu Ser Thr Gly Leu Val Glu Leu Gln Arg His
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 245 250 255
 Pro Met Phe Gln Pro Cys Val Val Pro Pro Lys Pro Trp Val Ala Ile
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 Ser Lys Lys Gly Leu Met Arg Tyr Glu Asp Val Tyr Met Pro Glu Val
 290 295 300
 Tyr Lys Ala Val Asn Leu Ala Gln Asn Thr Ala Trp Lys Ile Asn Lys
 305 310 315 320
 Lys Val Leu Ala Val Val Asn Glu Ile Val Asn Trp Lys Asn Cys Pro
 325 330 335
 Val Ala Asp Ile Pro Ser Leu Glu Arg Gln Glu Leu Pro Pro Lys Pro
 340 345 350
 Asp Asp Ile Asp Thr Asn Glu Ala Ala Leu Lys Glu Trp Lys Lys Ala
 355 360 365
 Ala Ala Gly Ile Tyr Arg Leu Asp Lys Ala Arg Val Ser Arg Arg Ile
 370 375 380
 Ser Leu Glu Phe Met Leu Glu Gln Ala Asn Lys Phe Ala Ser Lys Lys
 385 390 395 400
 Ala Ile Trp Phe Pro Tyr Asn Met Asp Trp Arg Gly Arg Val Tyr Ala
 405 410 415

Val Pro Met Phe Gly Asn Asp Met Thr Lys Gly Leu Leu Thr Leu Ala
 420 425 430
 Lys Gly Lys Pro Ile Gly Glu Glu Gly Phe Tyr Trp Leu Lys Ile His
 435 440 445
 Gly Ala Asn Cys Ala Gly Val Asp Lys Val Pro Phe Pro Glu Arg Ile
 450 455 460
 Ala Phe Ile Glu Lys His Val Asp Asp Ile Leu Ala Cys Ala Lys Asp
 465 470 475 480
 Pro Ile Asn Asn Thr Trp Trp Ala Glu Gln Asp Ser Pro Phe Ala Phe
 485 490 495
 Cys Phe Glu Tyr Ala Gly Val Thr His His Gly Leu Ser Tyr Asn Cys
 500 505 510
 Ser Leu Pro Leu Ala Phe Asp Gly Ser Cys Ser Gly Ile Gln His Phe
 515 520 525
 Ser Ala Met Leu Arg Asp Glu Val Gly Gly Arg Ala Val Asn Leu Leu
 530 535 540
 Pro Ser Glu Thr Val Gln Asp Ile Tyr Gly Ile Val Ala Gln Lys Val
 545 550 555 560
 Asn Glu Ile Leu Lys Gln Asn Gly Thr Pro Asn Glu Met Ile Thr Val
 565 570 575
 Thr Asp Lys Asp Thr Gly Glu Ile Ser Glu Lys Leu Lys Leu Gly Thr
 580 585 590
 Ser Thr Leu Ala Gln Gln Trp Leu Ala Tyr Gly Val Thr Arg Ser Val
 595 600 605
 Thr Lys Arg Ser Val Met Thr Leu Ala Tyr Gly Ser Lys Glu Phe Gly
 610 615 620
 Phe Arg Gln Gln Val Leu Asp Asp Thr Ile Gln Pro Ala Ile Asp Ser
 625 630 635 640
 Gly Lys Phe Thr Gln Pro Asn Gln Ala Ala Gly Tyr Met Ala Lys Leu
 645 650 655
 Ile Trp Asp Ala Val Ser Val Thr Val Val Ala Ala Val Glu Ala Met
 660 665 670
 Asn Trp Leu Lys Ser Ala Ala Lys Leu Leu Ala Ala Glu Val Lys Asp
 675 680 685
 Lys Lys Thr Lys Glu Ile Leu Arg His Arg Cys Ala Val His Trp Thr
 690 695 700
 Thr Pro Asp Gly Phe Pro Val Trp Gln Glu Pro Leu Gln Lys Arg Leu
 705 710 715 720

Asp Met Ile Phe Leu Gly Gln Phe Arg Leu Gln Pro Thr Ile Asn Thr
 725 730 735
 Leu Lys Asp Ser Gly Ile Asp Ala His Lys Gln Glu Ser Gly Ile Ala
 740 745 750
 Pro Asn Phe Val His Ser Gln Asp Gly Ser Arg Leu Met Thr Val Val
 755 760 765
 Tyr Ala His Glu Lys Tyr Gly Ile Glu Ser Phe Ala Leu Ile His Asp
 770 775 780
 Ser Phe Gly Thr Ile Pro Gly Lys Leu Phe Lys Ala Val Arg Glu Thr
 785 790 795 800
 Met Val Ile Thr Tyr Glu Asn Asn Asp Val Leu Ala Asp Phe Tyr Ser
 805 810 815
 Gln Phe Ala Asp Gln Leu His Glu Thr Gln Leu Asp Lys Met Pro Pro
 820 825 830
 Leu Pro Lys Lys Gly Asn Leu Asn Leu Gln Asp Ile Leu Lys Ser Asp
 835 840 845
 Phe Ala Phe Ala
 850

<210> 5
 <211> 876
 <212> PRT
 <213> Bacteriophage K11

<400> 5
 Met Asn Ala Leu Asn Ile Gly Arg Asn Asp Phe Ser Glu Ile Glu Leu
 1 5 10 15
 Ala Ala Ile Pro Tyr Asn Ile Leu Ser Glu His Tyr Gly Asp Gln Ala
 20 25 30
 Ala Arg Glu Gln Leu Ala Leu Glu His Glu Ala Tyr Glu Leu Gly Arg
 35 40 45
 Gln Arg Phe Leu Lys Met Leu Glu Arg Gln Val Lys Ala Gly Glu Phe
 50 55 60
 Ala Asp Asn Ala Ala Lys Pro Leu Val Leu Thr Gln Leu Thr Lys
 65 70 75 80
 Arg Ile Asp Asp Trp Lys Glu Glu Gln Ala Asn Ala Arg Gly Lys Lys
 85 90 95
 Pro Arg Ala Tyr Tyr Pro Ile Lys His Gly Val Ala Ser Glu Leu Ala
 100 105 110
 Val Ser Met Gly Ala Glu Val Leu Lys Glu Lys Arg Gly Val Ser Ser
 115 120 125

Glu Ala Ile Ala Leu Leu Thr Ile Lys Val Val Leu Gly Asn Ala His
 130 135 140
 Arg Pro Leu Lys Gly His Asn Pro Ala Gln Leu Gly Lys Ala Leu Glu
 145 150 155 160
 Asp Glu Ala Arg Phe Gly Arg Ile Arg Glu Gln Glu Ala Ala Tyr Phe
 165 170 175
 Lys Lys Asn Val Ala Asp Gln Leu Asp Lys Arg Val Gly His Val Tyr
 180 185 190
 Lys Lys Ala Phe Met Gln Val Val Glu Ala Asp Met Ile Ser Lys Gly
 195 200 205
 Met Leu Gly Gly Asp Asn Trp Ala Ser Trp Lys Thr Asp Glu Gln Met
 210 215 220
 His Val Gly Thr Lys Leu Leu Ile Glu Gly Thr Gly Leu Val Glu Met
 225 230 235 240
 Thr Lys Asn Lys Met Ala Asp Gly Ser Asp Asp Val Thr Ser Met Gln
 245 250 255
 Met Val Gln Leu Ala Pro Ala Phe Val Glu Leu Leu Ser Lys Arg Ala
 260 265 270
 Gly Ala Leu Ala Gly Ile Ser Pro Met His Gln Pro Cys Val Val Pro
 275 280 285
 Pro Lys Pro Trp Val Glu Thr Val Gly Gly Tyr Trp Ser Val Gly
 290 295 300
 Leu Ala Leu Val Arg Thr His Ser Lys Lys Ala Leu Arg Arg Tyr Ala
 305 310 315 320
 Asp Val His Met Pro Glu Val Tyr Lys Ala Val Asn Leu Ala Gln Asn
 325 330 335
 Thr Pro Trp Lys Val Asn Lys Val Leu Ala Val Val Asn Glu Ile
 340 345 350
 Val Asn Trp Lys His Cys Pro Val Gly Asp Val Pro Ala Ile Glu Arg
 355 360 365
 Glu Glu Leu Pro Pro Arg Pro Asp Asp Ile Asp Thr Asn Glu Val Ala
 370 375 380
 Arg Lys Ala Trp Arg Lys Glu Ala Ala Ala Val Tyr Arg Lys Asp Lys
 385 390 395 400
 Ala Arg Gln Ser Arg Arg Cys Arg Cys Glu Phe Met Val Ala Gln Ala
 405 410 415
 Asn Lys Phe Ala Asn His Lys Ala Ile Trp Phe Pro Tyr Asn Met Asp
 420 425 430

Trp Arg Gly Arg Val Tyr Ala Val Ser Met Phe Gly Asn Asp Met Thr
 435 440 445
 Lys Gly Ser Leu Thr Leu Ala Lys Gly Lys Pro Ile Gly Leu Asp Gly
 450 455 460
 Phe Tyr Trp Leu Lys Ile His Gly Ala Asn Cys Ala Gly Val Asp Lys
 465 470 475 480
 Val Pro Phe Pro Glu Arg Ile Lys Phe Ile Glu Glu Asn Glu Gly Asn
 485 490 495
 Ile Leu Ala Ser Ala Ala Asp Pro Leu Asn Thr Trp Trp Thr Gln Gln
 500 505 510
 Asp Ser Pro Phe Ala Phe Cys Phe Glu Tyr Ala Gly Val Lys His His
 515 520 525
 Gly Leu Asn Ser Tyr Asn Cys Ser Leu Pro Leu Ala Phe Asp Gly Ser
 530 535 540
 Cys Ser Gly Ile Gln His Phe Ser Ala Met Leu Arg Asp Glu Val Gly
 545 550 555 560
 Gly Arg Ala Val Asn Leu Leu Pro Ser Asp Thr Val Asp Ile Tyr Lys
 565 570 575
 Ile Val Ala Asp Lys Val Asn Glu Val Leu His Gln Asn Gly Ser Gln
 580 585 590
 Thr Val Val Glu Gln Ile Ala Asp Lys Glu Thr Gly Glu Phe His Glu
 595 600 605
 Lys Val Thr Leu Gly Glu Ser Val Leu Ala Ala Gly Gln Trp Leu Gln
 610 615 620
 Tyr Gly Val Thr Arg Lys Val Thr Lys Arg Ser Val Met Thr Leu Ala
 625 630 635 640
 Tyr Gly Ser Lys Glu Ser Leu Val Arg Gln Gln Val Leu Glu Asp Thr
 645 650 655
 Ile Gln Pro Ala Ile Asp Asn Gly Glu Phe Thr His Gln Pro Asn Gln
 660 665 670
 Ala Ala Gly Tyr Met Ala Lys Leu Ile Asp Ala Ser Thr Ser Val Thr
 675 680 685
 Val Val Ala Ala Val Glu Ala Met Asn Trp Leu Lys Ser Ala Ala Lys
 690 695 700
 Leu Leu Ala Ala Glu Val Lys Asp Lys Lys Gly Val Ile Leu His
 705 710 715 720
 Arg Cys Ala Val His Trp Val Thr Pro Asp Gly Phe Pro Val Trp Gln
 725 730 735

Glu Gln Asn Gln Ala Arg Leu Lys Leu Val Phe Leu Gly Gln Ala Asn
 740 745 750

Val Lys Met Thr Tyr Asn Thr Gly Lys Asp Ser Glu Ile Asp Ala His
 755 760 765

Lys Gln Glu Ser Gly Ile Ala Pro Asn Phe Val His Ser Gln Asp Gly
 770 775 780

Ser His Leu Arg Met Thr Val Val His Ala Asn Glu Val Tyr Gly Ile
 785 790 795 800

Asp Ser Phe Ala Leu Ile His Asp Ser Phe Gly Thr Ile Pro Gly Asn
 805 810 815

Leu Phe Lys Ala Val Arg Glu Thr Met Val Lys Thr Tyr Glu Asp Asn
 820 825 830

Asp Val Ile Ala Asp Phe Tyr Asp Gln Phe Ala Asp Gln Leu His Glu
 835 840 845

Ser Gln Leu Asp Lys Met Pro Ala Val Pro Ala Lys Gly Asp Leu Asn
 850 855 860

Leu Arg Asp Ile Leu Glu Ser Asp Phe Ala Phe Ala
 865 870 875

<210> 6

<211> 841

<212> PRT

<213> Bacteriophage SP6

<400> 6

Met Gln Asp Leu His Ala Ile Gln Leu Gln Leu Glu Glu Glu Met Phe
 1 5 10 15

Asn Gly Gly Ile Arg Arg Phe Glu Ala Asp Gln Gln Arg Gln Ile Ala
 20 25 30

Ala Gly Ser Glu Ser Asp Thr Ala Trp Asn Arg Arg Leu Leu Ser Glu
 35 40 45

Pro Met Ala Glu Gly Ile Gln Ala Tyr Lys Glu Glu Tyr Glu Gly Lys
 50 55 60

Lys Gly Arg Ala Pro Arg Ala Leu Ala Phe Leu Gln Cys Val Glu Asn
 65 70 75 80

Glu Val Ala Ala Tyr Ile Thr Met Lys Val Val Met Asp Met Leu Asn
 85 90 95

Thr Asp Ala Thr Leu Gln Ser Val Ala Glu Arg Ile Glu Asp Gln Val
 100 105 110

Arg Phe Ser Lys Leu Glu Gly His Ala Ala Lys Tyr Phe Glu Lys Val
 115 120 125

Lys Lys Ser Leu Lys Ala Ser Arg Thr Lys Ser Tyr Arg His Ala His
 130 135 140
 Asn Val Ala Val Val Ala Glu Lys Ser Val Ala Glu Lys Asp Ala Asp
 145 150 155 160
 Phe Asp Arg Trp Glu Ala Trp Pro Lys Glu Thr Gln Leu Gln Ile Gly
 165 170 175
 Thr Thr Ile Leu Glu Gly Ser Val Phe Tyr Asn Gly Glu Pro Val Phe
 180 185 190
 Met Arg Ala Met Arg Thr Tyr Gly Gly Lys Thr Ile Tyr Tyr Leu Gln
 195 200 205
 Thr Ser Glu Ser Val Gly Gln Trp Ile Ser Ala Phe Lys Glu His Val
 210 215 220
 Ala Gln Leu Ser Pro Ala Tyr Ala Pro Cys Val Ile Pro Pro Arg Pro
 225 230 235 240
 Trp Arg Thr Pro Phe Asn Gly Gly Phe His Thr Glu Lys Val Ile Arg
 245 250 255
 Leu Val Lys Gly Asn Arg Glu His Val Arg Lys Leu Thr Gln Lys Gln
 260 265 270
 Met Pro Lys Val Tyr Lys Ala Ile Asn Ala Leu Gln Asn Thr Gln Trp
 275 280 285
 Gln Ile Asn Lys Asp Val Leu Ala Val Ile Glu Glu Val Ile Arg Leu
 290 295 300
 Asp Leu Gly Tyr Gly Val Pro Ser Phe Lys Pro Leu Ile Asp Lys Glu
 305 310 315 320
 Asn Lys Pro Ala Asn Pro Val Pro Val Glu Leu Arg Gly Arg Glu Leu
 325 330 335
 Lys Glu Met Leu Ser Pro Glu Gln Trp Gln Gln Phe Ile Asn Trp Lys
 340 345 350
 Gly Glu Cys Ala Arg Leu Tyr Thr Ala Glu Thr Lys Arg Gly Ser Lys
 355 360 365
 Ser Ala Ala Val Val Arg Met Val Gly Gln Ala Arg Lys Tyr Ser Ala
 370 375 380
 Phe Glu Ser Ile Tyr Phe Val Tyr Ala Met Asp Ser Arg Ser Arg Val
 385 390 395 400
 Tyr Val Gln Ser Ser Thr Leu Ser Asn Asp Leu Gly Lys Ala Leu Leu
 405 410 415
 Arg Phe Thr Glu Gly Arg Pro Val Asn Gly Val Glu Ala Leu Lys Trp
 420 425 430

Phe Cys Ile Asn Gly Ala Asn Leu Trp Gly Trp Asp Lys Lys Thr Phe
 435 440 445
 Asp Val Arg Val Ser Asn Val Leu Asp Glu Glu Phe Gln Asp Met Cys
 450 455 460
 Arg Asp Ile Ala Ala Asp Pro Leu Thr Phe Thr Gln Trp Ala Lys Ala
 465 470 475 480
 Asp Ala Pro Tyr Ala Trp Cys Phe Glu Tyr Ala Gln Tyr Leu Asp Leu
 485 490 495
 Val Asp Glu Gly Arg Ala Asp Glu Phe Arg Thr His Leu Pro Val His
 500 505 510
 Gln Asp Gly Ser Cys Ser Gly Ile Gln His Tyr Ser Ala Met Leu Arg
 515 520 525
 Asp Glu Val Gly Ala Lys Ala Val Asn Leu Lys Pro Ser Asp Ala Pro
 530 535 540
 Gln Asp Ile Tyr Gly Ala Val Ala Gln Val Val Ile Asn Ala Leu Tyr
 545 550 555 560
 Met Asp Ala Asp Asp Ala Thr Thr Phe Thr Ser Gly Ser Val Thr Leu
 565 570 575
 Ser Gly Thr Glu Leu Arg Ala Met Ala Ser Ala Trp Asp Ser Ile Gly
 580 585 590
 Ile Thr Arg Ser Leu Thr Lys Lys Pro Val Met Thr Leu Pro Tyr Gly
 595 600 605
 Ser Thr Arg Leu Thr Cys Arg Glu Ser Val Ile Asp Tyr Ile Val Asp
 610 615 620
 Leu Glu Glu Lys Glu Ala Gln Lys Glu Gly Arg Thr Ala Asn Lys Val
 625 630 635 640
 His Pro Phe Glu Asp Asp Arg Gln Asp Tyr Leu Thr Pro Gly Ala Ala
 645 650 655
 Tyr Asn Tyr Met Thr Ala Leu Ile Trp Pro Ser Ile Ser Glu Val Val
 660 665 670
 Lys Ala Pro Ile Val Ala Met Lys Met Ile Arg Gln Leu Ala Arg Phe
 675 680 685
 Ala Ala Lys Arg Asn Glu Gly Leu Met Tyr Thr Leu Pro Thr Gly Phe
 690 695 700
 Ile Leu Glu Gln Lys Thr Glu Met Leu Arg Val Arg Thr Cys Leu Met
 705 710 715 720
 Gly Asp Ile Lys Met Ser Leu Gln Val Glu Thr Asp Ile Val Asp Glu
 725 730 735

Ala Ala Met Met Gly Ala Ala Ala Pro Asn Phe Val His Gly His Asp
 740 745 750

Ala Ser His Leu Ile Leu Thr Val Cys Glu Leu Val Asp Lys Gly Val
 755 760 765

Thr Ser Ile Ala Val Ile His Asp Ser Phe Gly Thr His Ala Leu Thr
 770 775 780

Leu Arg Val Ala Leu Lys Gly Gln Met Val Ala Met Tyr Ile Asp Gly
 785 790 795 800

Asn Ala Leu Gln Lys Leu Leu Glu Glu His Glu Val Arg Trp Met Val
 805 810 815

Asp Thr Gly Ile Glu Val Pro Glu Gln Gly Glu Phe Asp Leu Asn Glu
 820 825 830

Ile Met Asp Ser Glu Tyr Val Phe Ala
 835 840

<210> 7

<211> 78

<212> PRT

<213> Bacteriophage T7

<400> 7

Tyr Gly Val Thr Arg Ser Val Thr Lys Arg Ser Val Met Thr Leu Ala
 1 5 10 15

Tyr Gly Ser Lys Glu Phe Gly Phe Arg Gln Gln Val Leu Glu Asp Thr
 20 25 30

Ile Gln Pro Ala Ile Asp Ser Gly Lys Gly Leu Met Phe Thr Gln Pro
 35 40 45

Asn Gln Ala Ala Gly Tyr Met Ala Lys Leu Ile Trp Glu Ser Val Ser
 50 55 60

Val Thr Val Val Ala Ala Val Glu Ala Met Asn Trp Leu Lys
 65 70 75

<210> 8

<211> 78

<212> PRT

<213> Bacteriophage T7

<220>

<221> PEPTIDE

<222> (1)..(78)

<223> Mutant T7 RNA polymerase F644Y.

<400> 8

Tyr Gly Val Thr Arg Ser Val Thr Lys Arg Ser Val Met Thr Leu Ala
 1 5 10 15

Tyr Gly Ser Lys Glu Tyr Gly Phe Arg Gln Gln Val Leu Glu Asp Thr
 20 25 30

Ile Gln Pro Ala Ile Asp Ser Gly Lys Gly Leu Met Phe Thr Gln Pro
 35 40 45

Asn Gln Ala Ala Gly Tyr Met Ala Lys Leu Thr Trp Glu Ser Val Ser
 50 55 60

Val Thr Val Val Ala Ala Val Glu Ala Met Asn Trp Leu Lys
 65 70 75

<210> 9

<211> 78

<212> PRT

<213> Bacteriophage T7

<220>

<221> PEPTIDE

<222> (1)..(78)

<223> Mutant T7 RNA polymerase F646Y.

<400> 9

Tyr Gly Val Thr Arg Ser Val Thr Lys Arg Ser Val Met Thr Leu Ala
 1 5 10 15

Tyr Gly Ser Lys Glu Phe Gly Tyr Arg Gln Gln Val Leu Glu Asp Thr
 20 25 30

Ile Gln Pro Ala Ile Asp Ser Gly Lys Gly Leu Met Phe Thr Gln Pro
 35 40 45

Asn Gln Ala Ala Gly Tyr Met Ala Lys Leu Ile Trp Glu Ser Val Ser
 50 55 60

Val Thr Val Val Ala Ala Val Glu Ala Met Asn Trp Leu Lys
 65 70 75

<210> 10

<211> 78

<212> PRT

<213> Bacteriophage T7

<220>

<221> PEPTIDE

<222> (1)..(78)

<223> Mutant T7 RNA polymerase L665P/F667Y.

<400> 10

Tyr Gly Val Thr Arg Ser Val Thr Lys Arg Ser Val Met Thr Leu Ala
 1 5 10 15

Tyr Gly Ser Lys Glu Phe Gly Phe Arg Gln Gln Val Leu Glu Asp Thr
 20 25 30

Ile Gln Pro Ala Ile Asp Ser Gly Lys Gly Pro Met Tyr Thr Gln Pro
 35 40 45

Asn Gln Ala Ala Gly Tyr Met Ala Lys Leu Ile Trp Glu Ser Val Ser
 50 55 60

Val Thr Val Val Ala Ala Val Glu Ala Met Asn Trp Leu Lys
 65 70 75

<210> 11
 <211> 73
 <212> PRT
 <213> Bacteriophage T7

<400> 11
 Ala Gly Gln Trp Leu Ala Tyr Gly Val Thr Arg Ser Val Thr Lys Arg
 1 5 10 15

Ser Val Met Thr Leu Ala Tyr Gly Ser Lys Glu Phe Gly Phe Arg Gln
 20 25 30

Gln Val Leu Glu Asp Thr Ile Gln Pro Ala Ile Asp Ser Gly Lys Gly
 35 40 45

Leu Met Phe Thr Gln Pro Asn Gln Ala Ala Gly Tyr Met Ala Lys Leu
 50 55 60

Ile Trp Glu Ser Val Ser Val Thr Val
 65 70

<210> 12
 <211> 73
 <212> PRT
 <213> Bacteriophage T7

<220>
 <221> PEPTIDE
 <222> (1)..(73)
 <223> Mutant T7 RNA polymerase F644Y.

<400> 12
 Ala Gly Gln Trp Leu Ala Tyr Gly Val Thr Arg Ser Val Thr Lys Arg
 1 5 10 15

Ser Val Met Thr Leu Ala Tyr Gly Ser Lys Glu Tyr Gly Phe Arg Gln
 20 25 30

Gln Val Leu Glu Asp Thr Ile Gln Pro Ala Ile Asp Ser Gly Lys Gly
 35 40 45

Leu Met Phe Thr Gln Pro Asn Gln Ala Ala Gly Tyr Met Ala Lys Leu
 50 55 60

Ile Trp Glu Ser Val Ser Val Thr Val
 65 70

<210> 13
 <211> 73
 <212> PRT
 <213> Bacteriophage T7

<220>
 <221> PEPTIDE
 <222> (1)..(73)
 <223> Mutant T7 RNA polymerase L665P/F667Y.

<400> 13
 Ala Gly Gln Trp Leu Ala Tyr Gly Val Thr Arg Ser Val Thr Lys Arg
 1 5 10 15

Ser Val Met Thr Leu Ala Tyr Gly Ser Lys Glu Phe Gly Phe Arg Gln
 20 25 30

Gln Val Leu Glu Asp Thr Ile Gln Pro Ala Ile Asp Ser Gly Lys Gly
 35 40 45

Pro Met Tyr Thr Gln Pro Asn Gln Ala Ala Gly Tyr Met Ala Lys Leu
 50 55 60

Ile Trp Glu Ser Val Ser Val Thr Val
 65 70

<210> 14
 <211> 73
 <212> PRT
 <213> Bacteriophage T3

<400> 14
 Ala Gln Gln Trp Leu Ala Tyr Gly Val Thr Arg Ser Val Thr Lys Arg
 1 5 10 15

Ser Val Met Thr Leu Ala Tyr Gly Ser Lys Glu Phe Gly Phe Arg Gln
 20 25 30

Gln Val Leu Asp Asp Thr Ile Gln Pro Ala Ile Asp Ser Gly Lys Gly
 35 40 45

Leu Met Phe Thr Gln Pro Asn Gln Ala Ala Gly Tyr Met Ala Lys Leu
 50 55 60

Ile Trp Asp Ala Val Ser Val Thr Val
 65 70

<210> 15
 <211> 73
 <212> PRT
 <213> Bacteriophage K11

<400> 15
 Ala Ala Gln Trp Leu Gln Tyr Gly Val Thr Arg Lys Val Thr Lys Arg
 1 5 10 15

Ser Val Met Thr Leu Ala Tyr Gly Ser Lys Glu Ser Leu Val Arg Gln
 20 25 30

Gln Val Leu Glu Asp Thr Ile Gln Pro Ala Ile Asp Asn Gly Glu Gly
 35 40 45

Leu Met Phe Thr His Pro Asn Gln Ala Ala Gly Tyr Met Ala Lys Leu
 50 55 60

Ile Trp Asp Ala Val Thr Val Thr Val
 65 70

<210> 16

<211> 75

<212> PRT <

213> Bacteriophage SP6

<400> 16

Ala Ser Ala Trp Asp Ser Ile Gly Ile Thr Arg Ser Leu Thr Lys Lys
 1 5 10 15

Pro Val Met Thr Leu Pro Tyr Gly Ser Thr Arg Leu Thr Cys Arg Glu
 20 25 30

Ser Val Ile Asp Tyr Ile Val Asp Leu Glu Glu Lys Glu Ala Gln Lys
 35 40 45

Ala Val Ala Glu Gly Arg Thr Ala Asn Lys Val His Pro Phe Glu Asp
 50 55 60

Asp Arg Gln Asp Tyr Leu Thr Pro Gly Ala Ala
 65 70 75

<210> 17

<211> 31

<212> DNA

<213> Bacteriophage T7

<220>

<221> misc_feature

<222> (1)..(31)

<223> Mutant T7 RNA polymerase wild type.

<220>

<221> misc_feature

<222> (25)..(25)

<223> Nucleotide 25 is "n" wherein "n" = any nucleotide.

<400> 17

gggaggggggg gggggggggcc ccccnngggcg t

31

<210> 18

<211> 32

<212> DNA

<213> Bacteriophage T7

<220>

<221> misc_feature

<222> (1)..(32)

<223> Mutant T7 RNA polymerase wild type.

<220>

<221> misc_feature

<222> (1)..(32)

<223> Nucleotides 6-8, 18, 25-30 are "n" wherein "n" = any nucleotide.

<400> 18

gcgtcnnnaa aacgcacntt ttctntcgtt gg

32

<210> 19

<211> 19

<212> DNA

<213> Bacteriophage T7

<220>

<221> misc_feature

<222> (1)..(19)

<223> Mutant T7 RNA polymerase F644Y.

<400> 19

cgaggggggg ccggtagcc

19

<210> 20

<211> 25

<212> DNA

<213> Bacteriophage T7

<220>

<221> misc_feature

<222> (1)..(25)

<223> Mutant T7 RNA polymerase F644Y.

<220>

<221> misc_feature

<222> (6)..(6)

<223> Nucleotide 6 is "n" wherein "n" = any nucleotide.

<400> 20

ccctnttttg ttccttttagt gaggt

25

<210> 21

<211> 18

<212> DNA

<213> Bacteriophage T7

<220>

<221> misc_feature

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<222> (1)..(18)
<223> Mutant T7 RNA polymerase F667Y.

<400> 21
gagggggggcc ggttaacgc 18

<210> 22
<211> 22
<212> DNA
<213> Bacteriophage T7

<220>
<221> misc_feature
<222> (1)..(22)
<223> Mutant T7 RNA polymerase F667Y.

<400> 22
acgccttttg ttcccttttag tg 22

<210> 23
<211> 569
<212> DNA
<213> Bacteriophage T7
<220>
<221> misc_feature
<222> (1)..(569)
<223> Mutant T7 RNA polymerase F644Y/L665P/F667Y.

<220>
<221> misc_feature
<222> (1)..(472)
<223> Nucleotides 1-14, 17-18, 21, 26, 29, 34, 38, 40, 50-51, 53, 58, 7
      5-76, 85, 110, 117, 132, 142, 150, 157, 399, 440 and 472 are "n"
      wherein "n" = any nucleotide

<400> 23
nnnnnnnnnnnnnnnnngt ngtttncgna tccnaaangn aacaggggn nantgtgnaa 60
acatgaatat ttttnntaag ctttnattcc agggcaagac attttaaccn aaattgncaa
attatatcac tnatttagaca gaaaaatctn acccagntaa gacttctgga gttttggtag
agtagtttgt cttggatgct tcatgtatgc agtcacttat agtcagtatt gcacttggca
cacttcagct taaaccaaca ggtatggaaa aatagggagc aacatggagt ggcacatcctgg
tatttctaca gtcctgtaga tgaagtctct atatgtgcaa catcctggga cagagcatat
ttgggaagaa acagtttgcc attgaatccc gtgtcatana atatccagca cagatggtag
tggatgggt tagcaataan cacactctct ctttcgatg tgcattgtat antcaggtgg
ataaaaaaaag acatcgcttg gcccacatgc aaggccaaaaa agcagacatc agaaagagag
cagtcatgtg gggaaattgg tccgactgc 540
                                         569

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